

SEQUENCE LISTING

5 <110> AGY Therapeutics
Melcher, Thorsten
10 Mueller, Sabine
Chin, Daniel

15 <120> USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION
OF BRAIN TUMORS

20 <130> 263/180 -- PEagleman -- AGY

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30 <170> PatentIn version 3.1

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Tyr Arg Gln Gln Arg Lys Leu Val Glu Glu Ile Gly Trp Ser Tyr Thr
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8058

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35 Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
35 40 45
40 Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
50 55 60
45 Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
65 70 75 80
Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
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50 Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
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55 Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
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10 Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
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15 Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
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20 Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
180 185 190

25 Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
195 200 205

30 Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
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35 Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
225 230 235 240

40 Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
245 250 255

45 Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
260 265 270

50 Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
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55 Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
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60 Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
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65 Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
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70 Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
340 345 350

5 Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
355 360 365

10 Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
370 375 380

15 Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
385 390 395 400

20 Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
405 410 415

25 Leu Phe Pro Glu Leu Ile Gly Thr Glu Glu Ile Ile Lys Glu Glu Glu
420 425 430

30 Glu Gly Lys Asp Ile Glu Glu Gly Ala Ile Val Asn Pro Gly Arg Asp
435 440 445

35 Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
450 455 460

40 Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
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45 Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
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50 Asn Thr Ser Leu Asn Ser Thr Ser Gln Pro Val Thr Lys Leu Ala Thr
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55 Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro
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60 His Thr Val Glu Gly Thr Ser Ala Ser Leu Asn Asp Gly Ser Lys Thr
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65 Val Leu Arg Ser Pro His Met Asn Leu Ser Gly Thr Ala Glu Ser Leu
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70 Asn Thr Val Ser Ile Thr Glu Tyr Glu Glu Glu Ser Leu Leu Thr Ser
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5 Phe Lys Leu Asp Thr Gly Ala Glu Asp Ser Ser Gly Ser Ser Pro Ala
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10 Thr Ser Ala Ile Pro Phe Ile Ser Glu Asn Ile Ser Gln Gly Tyr Ile
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15 Phe Ser Ser Glu Asn Pro Glu Thr Ile Thr Tyr Asp Val Leu Ile Pro
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20 Glu Ser Ala Arg Asn Ala Ser Glu Asp Ser Thr Ser Ser Gly Ser Glu
625 630 635 640

25 Glu Ser Leu Lys Asp Pro Ser Met Glu Gly Asn Val Trp Phe Pro Ser
645 650 655

30 Ser Thr Asp Ile Thr Ala Gln Pro Asp Val Gly Ser Gly Arg Glu Ser
660 665 670

35 Phe Leu Gln Thr Asn Tyr Thr Glu Ile Arg Val Asp Glu Ser Glu Lys
675 680 685

40 Thr Thr Lys Ser Phe Ser Ala Gly Pro Val Met Ser Gln Gly Pro Ser
690 695 700

45 Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
705 710 715 720

50 Thr Glu Val Thr Pro His Ala Phe Thr Pro Ser Ser Arg Gln Gln Asp
725 730 735

55 Leu Val Ser Thr Val Asn Val Val Tyr Ser Gln Thr Thr Gln Pro Val
740 745 750

60 Tyr Asn Gly Glu Thr Pro Leu Gln Pro Ser Tyr Ser Ser Glu Val Phe
755 760 765

65 Pro Leu Val Thr Pro Leu Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
770 775 780

70 Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
785 790 795 800

5 Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
805 810 815

10 Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
820 825 830

15 Arg His Leu His Thr Val Ser Gln Ile Leu Pro Gln Val Thr Ser Ala
835 840 845

20 Thr Glu Ser Asp Lys Val Pro Leu His Ala Ser Leu Pro Val Ala Gly
850 855 860

25 Gly Asp Leu Leu Leu Glu Pro Ser Leu Ala Gln Tyr Ser Asp Val Leu
865 870 875 880

30 Ser Thr Thr His Ala Ala Ser Glu Thr Leu Glu Phe Gly Ser Glu Ser
885 890 895

35 Gly Val Leu Tyr Lys Thr Leu Met Phe Ser Gln Val Glu Pro Pro Ser
900 905 910

40 Ser Asp Ala Met Met His Ala Arg Ser Ser Gly Pro Glu Pro Ser Tyr
915 920 925

45 Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr
930 935 940

50 Ser Ser Ala Ile Pro Val His Asp Ser Val Gly Val Thr Tyr Gln Gly
945 950 955 960

55 Ser Leu Phe Ser Gly Pro Ser His Ile Pro Ile Pro Lys Ser Ser Leu
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60 Ile Thr Pro Thr Ala Ser Leu Leu Gln Pro Thr His Ala Leu Ser Gly
980 985 990

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70 Asp Thr Asp Gly Leu Thr Ala Leu Asn Ile Ser Ser Pro Val Ser
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20 Thr Val Met Pro Asn Met Tyr Asp Asn Val Asn Lys Leu Asn Ala
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25 Ser Leu Gln Glu Thr Ser Val Ser Ile Ser Ser Thr Lys Gly Met
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30 Phe Pro Gly Ser Leu Ala His Thr Thr Thr Lys Val Phe Asp His
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35 Glu Ile Ser Gln Val Pro Glu Asn Asn Phe Ser Val Gln Pro Thr
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40 His Thr Val Ser Gln Ala Ser Gly Asp Thr Ser Leu Lys Pro Val
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45 Leu Ser Ala Asn Ser Glu Pro Ala Ser Ser Asp Pro Ala Ser Ser
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50 Glu Met Leu Ser Pro Ser Thr Gln Leu Leu Phe Tyr Glu Thr Ser
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55 Ala Ser Phe Ser Thr Glu Val Leu Leu Gln Pro Ser Phe Gln Ala
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Ser Asp Pro Ile Leu Val Glu Thr Pro Lys Val Asp Lys Ile Ser
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Ser Thr Met Leu His Leu Ile Val Ser Asn Ser Ala Ser Ser Glu
1220 1225 1230

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Asn Met Leu His Ser Thr Ser Val Pro Val Phe Asp Val Ser Pro
1235 1240 1245

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Thr Ser His Met His Ser Ala Ser Leu Gln Gly Leu Thr Ile Ser
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Tyr Ala Ser Glu Lys Tyr Glu Pro Val Leu Leu Lys Ser Glu Ser
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Ser His Gln Val Val Pro Ser Leu Tyr Ser Asn Asp Glu Leu Phe
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Gln Thr Ala Asn Leu Glu Ile Asn Gln Ala His Pro Pro Lys Gly
1295 1300 1305

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Arg His Val Phe Ala Thr Pro Val Leu Ser Ile Asp Glu Pro Leu
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Asn Thr Leu Ile Asn Lys Leu Ile His Ser Asp Glu Ile Leu Thr
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Ser Thr Lys Ser Ser Val Thr Gly Lys Val Phe Ala Gly Ile Pro
1340 1345 1350

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Thr Val Ala Ser Asp Thr Phe Val Ser Thr Asp His Ser Val Pro
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Ile Gly Asn Gly His Val Ala Ile Thr Ala Val Ser Pro His Arg
1370 1375 1380

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Asp Gly Ser Val Thr Ser Thr Lys Leu Leu Phe Pro Ser Lys Ala
1385 1390 1395

Thr Ser Glu Leu Ser His Ser Ala Lys Ser Asp Ala Gly Leu Val
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Gly Gly Gly Glu Asp Gly Asp Thr Asp Asp Asp Gly Asp Asp Asp
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Asp Asp Arg Asp Ser Asp Gly Leu Ser Ile His Lys Cys Met Ser
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5 Cys Ser Ser Tyr Arg Glu Ser Gln Glu Lys Val Met Asn Asp Ser
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10 Asp Thr His Glu Asn Ser Leu Met Asp Gln Asn Asn Pro Ile Ser
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15 Tyr Ser Leu Ser Glu Asn Ser Glu Glu Asp Asn Arg Val Thr Ser
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20 Val Ser Ser Asp Ser Gln Thr Gly Met Asp Arg Ser Pro Gly Lys
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25 Ser Pro Ser Ala Asn Gly Leu Ser Gln Lys His Asn Asp Gly Lys
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30 Glu Glu Asn Asp Ile Gln Thr Gly Ser Ala Leu Leu Pro Leu Ser
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35 Pro Glu Ser Lys Ala Trp Ala Val Leu Thr Ser Asp Glu Glu Ser
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45 Ser Thr Asp Phe Ser Phe Ala Asp Thr Asn Glu Lys Asp Ala Asp
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50 Gly Ile Leu Ala Ala Gly Asp Ser Glu Ile Thr Pro Gly Phe Pro
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55 Gln Ser Pro Thr Ser Ser Val Thr Ser Glu Asn Ser Glu Val Phe
1595 1600 1605

60 His Val Ser Glu Ala Glu Ala Ser Asn Ser Ser His Glu Ser Arg
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65 Ile Gly Leu Ala Glu Gly Leu Glu Ser Glu Lys Lys Ala Val Ile
1625 1630 1635

70 Pro Leu Val Ile Val Ser Ala Leu Thr Phe Ile Cys Leu Val Val
1640 1645 1650

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Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val Leu Ala Tyr
1850 1855 1860

5 Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile Lys Lys
1865 1870 1875

10 Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln Tyr
1880 1885 1890

15 His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu
1895 1900 1905

20 Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His
1910 1915 1920

25 Ala Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg
1925 1930 1935

30 Thr Gly Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln
1940 1945 1950

35 His Glu Gly Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg
1955 1960 1965

40 Ser Gln Arg Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe
1970 1975 1980

45 Ile His Asp Thr Leu Val Glu Ala Ile Leu Ser Lys Glu Thr Glu
1985 1990 1995

50 Val Leu Asp Ser His Ile His Ala Tyr Val Asn Ala Leu Leu Ile
2000 2005 2010

55 Pro Gly Pro Ala Gly Lys Thr Lys Leu Glu Lys Gln Phe Gln Gly
2015 2020 2025

60 Leu Thr Leu Ser Pro Arg Leu Glu Cys Arg Gly Thr Ile Ser Ala
2030 2035 2040

65 His Cys Asn Leu Pro Leu Pro Gly Leu Thr Asp Pro Pro Thr Ser
2045 2050 2055

70 Ala Ser Arg Val Ala Gly Thr Ile Leu Leu Ser Gln Ser Asn Ile
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5 Gln Gln Ser Asp Tyr Ser Ala Ala Leu Lys Gln Cys Asn Arg Glu
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10 Lys Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser Arg Val
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20 Ser Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr
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25 Gln His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile
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30 Trp Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln
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35 Asn Met Ala Glu Asp Glu Phe Val Tyr Trp Pro Asn Lys Asp Glu
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40 Pro Ile Asn Cys Glu Ser Phe Lys Val Thr Leu Met Ala Glu Glu
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45 His Lys Cys Leu Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe
2195 2200 2205

50 Ile Leu Glu Ala Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His
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55 Phe Gln Cys Pro Lys Trp Pro Asn Pro Asp Ser Pro Ile Ser Lys
2225 2230 2235

Thr Phe Glu Leu Ile Ser Val Ile Lys Glu Glu Ala Ala Asn Arg
2240 2245 2250

Asp Gly Pro Met Ile Val His Asp Glu His Gly Gly Val Thr Ala
2255 2260 2265

Gly Thr Phe Cys Ala Leu Thr Thr Leu Met His Gln Leu Glu Lys
2270 2275 2280

Glu Asn Ser Val Asp Val Tyr Gln Val Ala Lys Met Ile Asn Leu
2285 2290 2295

Met Arg Pro Gly Val Phe Ala Asp Ile Glu Gln Tyr Gln Phe Leu
2300 2305 2310

Tyr Lys Val Ile Leu Ser Leu Val Ser Thr Arg Gln Glu Glu Asn
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Pro Ser Thr Ser Leu Asp Ser Asn Gly Ala Ala Leu Pro Asp Gly
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cgggcgagggg cgcgagaccg tctggaa atg cga atc cta aag cgt ttc ctc gct 174
Met Arg Ile Leu Lys Arg Phe Leu Ala
1 5

tgc att cag ctc ctc tgt gtt tgc cgc ctg gat tgg gct aat gga tac 222
Cys Ile Gln Leu Leu Cys Val Cys Arg Leu Asp Trp Ala Asn Gly Tyr
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Tyr Arg Gln Gln Arg Lys Leu Val Glu Glu Ile Gly Trp Ser Tyr Thr
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gga gca ctg aat caa aaa aat tgg gga aag aaa tat cca aca tgt aat 318
Gly Ala Leu Asn Gln Lys Asn Trp Gly Lys Lys Tyr Pro Thr Cys Asn
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agc cca aaa caa tct cct atc aat att gat gaa gat ctt aca caa gta 366
Ser Pro Lys Gln Ser Pro Ile Asn Ile Asp Glu Asp Leu Thr Gln Val
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aat gtg aat ctt aag aaa ctt aaa ttt cag ggt tgg gat aaa aca tca 414
Asn Val Asn Leu Lys Lys Leu Lys Phe Gln Gly Trp Asp Lys Thr Ser
75 80 85

ttg gaa aac aca ttc att cat aac act ggg aaa aca gtg gaa att aat 462
Leu Glu Asn Thr Phe Ile His Asn Thr Gly Lys Thr Val Glu Ile Asn
90 95 100 105

ctc act aat gac tac cgt gtc agc gga gga gtt tca gaa atg gtg ttt 510
Leu Thr Asn Asp Tyr Arg Val Ser Gly Gly Val Ser Glu Met Val Phe
110 115 120

aaa gca agc aag ata act ttt cac tgg gga aaa tgc aat atg tca tct 558
Lys Ala Ser Lys Ile Thr Phe His Trp Gly Lys Cys Asn Met Ser Ser
125 130 135

gat gga tca gag cat agt tta gaa gga caa aaa ttt cca ctt gag atg 606
Asp Gly Ser Glu His Ser Leu Glu Gly Gln Lys Phe Pro Leu Glu Met
140 145 150

caa atc tac tgc ttt gat gcg gac cga ttt tca agt ttt gag gaa gca 654
Gln Ile Tyr Cys Phe Asp Ala Asp Arg Phe Ser Ser Phe Glu Glu Ala
155 160 165

gtc aaa gga aaa ggg aag tta aga gct tta tcc att ttg ttt gag gtt 702
Val Lys Gly Lys Gly Lys Leu Arg Ala Leu Ser Ile Leu Phe Glu Val
170 175 180 185

ggg aca gaa gaa aat ttg gat ttc aaa gcg att att gat gga gtc gaa 750
Gly Thr Glu Glu Asn Leu Asp Phe Lys Ala Ile Ile Asp Gly Val Glu
190 195 200

agt gtt agt cgt ttt ggg aag cag gct gct tta gat cca ttc ata ctg 798
Ser Val Ser Arg Phe Gly Lys Gln Ala Ala Leu Asp Pro Phe Ile Leu
205 210 215

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ttg aac ctt ctg cca aac tca act gac aag tat tac att tac aat ggc 846
Leu Asn Leu Leu Pro Asn Ser Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly
220 225 230

tca ttg aca tct cct ccc tgc aca gac aca gtt gac tgg att gtt ttt 894
Ser Leu Thr Ser Pro Pro Cys Thr Asp Thr Val Asp Trp Ile Val Phe
235 240 245

aaa gat aca gtt agc atc tct gaa agc cag ttg gct gtt ttt tgt gaa 942
Lys Asp Thr Val Ser Ile Ser Glu Ser Gln Leu Ala Val Phe Cys Glu
250 255 260 265

gtt ctt aca atg caa caa tct ggt tat gtc atg ctg atg gac tac tta 990
Val Leu Thr Met Gln Gln Ser Gly Tyr Val Met Leu Met Asp Tyr Leu
270 275 280

caa aac aat ttt cga gag caa cag tac aag ttc tct aga cag gtg ttt 1038
Gln Asn Asn Phe Arg Glu Gln Gln Tyr Lys Phe Ser Arg Gln Val Phe
285 290 295

tcc tca tac act gga aag gaa gag att cat gaa gca gtt tgt agt tca 1086
Ser Ser Tyr Thr Gly Lys Glu Glu Ile His Glu Ala Val Cys Ser Ser
300 305 310

gaa cca gaa aat gtt cag gct gac cca gag aat tat acc agc ctt ctt 1134
Glu Pro Glu Asn Val Gln Ala Asp Pro Glu Asn Tyr Thr Ser Leu Leu
315 320 325

gtt aca tgg gaa aga cct cga gtc gtt tat gat acc atg att gag aag 1182
Val Thr Trp Glu Arg Pro Arg Val Val Tyr Asp Thr Met Ile Glu Lys
330 335 340 345

ttt gca gtt ttg tac cag cag ttg gat gga gag gac caa acc aag cat 1230
Phe Ala Val Leu Tyr Gln Gln Leu Asp Gly Glu Asp Gln Thr Lys His
350 355 360

gaa ttt ttg aca gat ggc tat caa gac ttg ggt gct att ctc aat aat 1278
Glu Phe Leu Thr Asp Gly Tyr Gln Asp Leu Gly Ala Ile Leu Asn Asn
365 370 375

ttg cta ccc aat atg agt tat gtt ctt cag ata gta gcc ata tgc act 1326
Leu Leu Pro Asn Met Ser Tyr Val Leu Gln Ile Val Ala Ile Cys Thr
380 385 390

aat ggc tta tat gga aaa tac agc gac caa ctg att gtc gac atg cct 1374
Asn Gly Leu Tyr Gly Lys Tyr Ser Asp Gln Leu Ile Val Asp Met Pro
395 400 405

act gat aat cct gaa ctt gat ctt ttc cct gaa tta att gga act gaa 1422
Thr Asp Asn Pro Glu Leu Asp Leu Phe Pro Glu Leu Ile Gly Thr Glu
410 415 420 425

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430 435 440

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Ile Val Asn Pro Gly Arg Asp Ser Ala Thr Asn Gln Ile Arg Lys Lys
445 450 455

10 gaa ccc cag att tct acc aca aca cac tac aat cgc ata ggg acg aaa 1566
Glu Pro Gln Ile Ser Thr Thr Thr His Tyr Asn Arg Ile Gly Thr Lys
460 465 470

15 tac aat gaa gcc aag act aac cga tcc cca aca aga gga agt gaa ttc 1614
Tyr Asn Glu Ala Lys Thr Asn Arg Ser Pro Thr Arg Gly Ser Glu Phe
475 480 485

20 tct gga aag ggt gat gtt ccc aat aca tct tta aat tcc act tcc caa 1662
Ser Gly Lys Gly Asp Val Pro Asn Thr Ser Leu Asn Ser Thr Ser Gln
490 495 500 505

25 cca gtc act aaa tta gcc aca gaa aaa gat att tcc ttg act tct cag 1710
Pro Val Thr Lys Leu Ala Thr Glu Lys Asp Ile Ser Leu Thr Ser Gln
510 515 520

30 act gtg act gaa ctg cca cct cac act gtg gaa ggt act tca gcc tct 1758
Thr Val Thr Glu Leu Pro Pro His Thr Val Glu Gly Thr Ser Ala Ser
525 530 535

35 tta aat gat ggc tct aaa act gtt ctt aga tct cca cat atg aac ttg 1806
Leu Asn Asp Gly Ser Lys Thr Val Leu Arg Ser Pro His Met Asn Leu
540 545 550

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Ser Gly Thr Ala Glu Ser Leu Asn Thr Val Ser Ile Thr Glu Tyr Glu
555 560 565

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570 575 580 585

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Ser Ser Gly Ser Ser Pro Ala Thr Ser Ala Ile Pro Phe Ile Ser Glu
590 595 600

55 aac ata tcc caa ggg tat ata ttt tcc tcc gaa aac cca gag aca ata 1998
Asn Ile Ser Gln Gly Tyr Ile Phe Ser Ser Glu Asn Pro Glu Thr Ile
605 610 615

60 aca tat gat gtc ctt ata cca gaa tct gct aga aat gct tcc gaa gat 2046
Thr Tyr Asp Val Leu Ile Pro Glu Ser Ala Arg Asn Ala Ser Glu Asp
620 625 630

65 tca act tca tca ggt tca gaa gaa tca cta aag gat cct tct atg gag 2094
Ser Thr Ser Ser Gly Ser Glu Glu Ser Leu Lys Asp Pro Ser Met Glu
635 640 645

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Gly Asn Val Trp Phe Pro Ser Ser Thr Asp Ile Thr Ala Gln Pro Asp
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Val Gly Ser Gly Arg Glu Ser Phe Leu Gln Thr Asn Tyr Thr Glu Ile
670 675 680

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cgt gtt gat gaa tct gag aag aca acc aag tcc ttt tct gca ggc cca 2238
Arg Val Asp Glu Ser Glu Lys Thr Thr Lys Ser Phe Ser Ala Gly Pro
685 690 695

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gtg atg tca cag ggt ccc tca gtt aca gat ctg gaa atg cca cat tat 2286
Val Met Ser Gln Gly Pro Ser Val Thr Asp Leu Glu Met Pro His Tyr
700 705 710

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tct acc ttt gcc tac ttc cca act gag gta aca cct cat gct ttt acc 2334
Ser Thr Phe Ala Tyr Phe Pro Thr Glu Val Thr Pro His Ala Phe Thr
715 720 725

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cca tcc tcc aga caa cag gat ttg gtc tcc acg gtc aac gtg gta tac 2382
Pro Ser Ser Arg Gln Gln Asp Leu Val Ser Thr Val Asn Val Val Tyr
730 735 740 745

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tcg cag aca acc caa ccg gta tac aat ggt gag aca cct ctt caa cct 2430
Ser Gln Thr Thr Gln Pro Val Tyr Asn Gly Glu Thr Pro Leu Gln Pro
750 755 760

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780 785 790

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875 880 885

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cac atc ttc act gtt tct tac agt tct gca ata cct gtg cat gat tct 3006
His Ile Phe Thr Val Ser Tyr Ser Ser Ala Ile Pro Val His Asp Ser
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955 960 965

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	Lys Val Phe Ala	Gly Ile Pro Thr Val	Ala Ser Asp Thr Phe	Val	
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	Ser Thr Asp His	Ser Val Pro Ile Gly	Asn Gly His Val Ala	Ile	
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	Thr Ala Val Ser	Pro His Arg Asp Gly	Ser Val Thr Ser Thr	Lys	
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	Ser Ile His Lys	Cys Met Ser Cys Ser	Ser Tyr Arg Glu Ser	Gln	
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	Glu Asp Asn Arg	Val Thr Ser Val Ser	Ser Asp Ser Gln Thr	Gly	
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	Gln Lys His Asn	Asp Gly Lys Glu Glu	Asn Asp Ile Gln Thr	Gly	
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Ser Ala Leu Leu Pro Leu Ser Pro Glu Ser Lys Ala Trp Ala Val
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1590 1595 1600

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Ser Pro Arg Val Ile Ser Thr Pro Pro Thr Pro Ile Phe Pro Ile
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Ser Asp Asp Val Gly Ala Ile Pro Ile Lys His Phe Pro Lys His
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Leu Gly Ile Thr 1740 Ala Asp Ser Ser Asn His Pro Asp Asn Lys His 1750

10 aag aat cga tac ata aat atc gtt gcc tat gat cat agc agg gtt 5445
Lys Asn Arg Tyr 1755 Ile Asn Ile Val Ala Tyr Asp His Ser Arg Val 1765

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Lys Leu Ala Gln 1770 Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp Tyr 1780

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25 att gct gcc caa ggc cca ctg aaa tcc aca gct gaa gat ttc tgg 5580
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45 agt gtg caa gtg ctt gcc tat tat act gtg agg aat ttt act cta 5760
Ser Val Gln Val 1860 Leu Ala Tyr Tyr Thr Val Arg Asn Phe Thr Leu 1870

50 aga aac aca aaa ata aaa aag ggc tcc cag aaa gga aga ccc agt 5805
Arg Asn Thr Lys 1875 Ile Lys Lys Gly Ser Gln Lys Gly Arg Pro Ser 1885

55 gga cgt gtg gtc aca cag tat cac tac acg cag tgg cct gac atg 5850
Gly Arg Val Val 1890 Thr Gln Tyr His Tyr Thr Gln Trp Pro Asp Met 1900

60 gga gta cca gag tac tcc ctg cca gtg ctg acc ttt gtg aga aag 5895
Gly Val Pro Glu 1905 Tyr Ser Leu Pro Val Leu Thr Phe Val Arg Lys 1915

65 gca gcc tat gcc aag cgc cat gca gtg ggg cct gtt gtc gtc cac 5940
Ala Ala Tyr Ala 1920 Lys Arg His Ala Val Gly Pro Val Val Val His 1930

70 tgc agt gct gga gtt gga aga aca ggc aca tat att gtg cta gac 5985
Cys Ser Ala Gly 1935 Val Gly Arg Thr Gly Thr Tyr Ile Val Leu Asp 1945

5 agt atg ttg cag cag att caa cac gaa gga act gtc aac ata ttt 6030
Ser Met Leu Gln Gln Ile Gln His Glu Gly Thr Val Asn Ile Phe
1950 1955 1960

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Gly Phe Leu Lys His Ile Arg Ser Gln Arg Asn Tyr Leu Val Gln
1965 1970 1975

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2010 2015 2020

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<222> (1)..(2314)

<223> Krueger, N.X. and Saito, H.: A human transmembrane protein-tyrosine-phosphatase, PTP zeta, is expressed in brain and has an N-terminal receptor domain homologous to carbonic anhydrases; Proc. Natl. Acad. Sci. USA 89 (16), 7417-7421 (1992)

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<222> (1)..(2314)

<223> PTP-zeta

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<221> Reference

<222> (1)..(2314)

<223> Levy, J.B., et al.; The cloning of a receptor-type protein tyrosine phosphatase expressed in the central nervous system; J. Biol. Chem. 268 (14), 10573-10581 (1993)

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<222> (755)..(1614)
<223> Splicing variant; missing (in short isoform)
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<221> BINDING
<222> (997)..(997)
<223> Chondroitin sulfate (potential)
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<223> Glycosylation; N-linked (GLCNAC...) (potential)

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10 <223> Glycosylation; N-linked (GLCNAC...) (potential)

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50 <223> Chondroitin sulfate (potential)

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<223> Chondroitin sulfate (potential)

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<222> (1617)..(1617)

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<222> (1636)..(1661)

<223> Transmembrane region; potential

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<222> (1662)..(2314)

<223> Cytoplasmic (potential)

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<222> (1722)..(1728)

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<222> (1932) .. (1932)

<223> Active site; by similarity

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<221> DOMAIN

<222> (1998) .. (2314)

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<222> (2222) .. (2222)

<223> Ancestral active site

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Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile

50

55

60

5 Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
65 70 75 80

10

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
85 90 95

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Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
100 105 110

Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
115 120 125

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His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
130 135 140

25

Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
145 150 155 160

30

Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
165 170 175

35

Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
180 185 190

Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
195 200 205

40

Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
210 215 220

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Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
225 230 235 240

50

Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
245 250 255

Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
260 265 270

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Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln

275 280 285

5 Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
290 295 300

10 Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
305 310 315 320

15 Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
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20 Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
340 345 350

25 Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
355 360 365

30 Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
370 375 380

35 Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
385 390 395 400

40 Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
405 410 415

45 Leu Phe Pro Glu Leu Ile Gly Thr Glu Glu Ile Ile Lys Glu Glu Glu
420 425 430

50 Glu Gly Lys Asp Ile Glu Glu Gly Ala Ile Val Asn Pro Gly Arg Asp
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55 Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
450 455 460

Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
465 470 475 480

Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
485 490 495

Asn Thr Ser Leu Asn Ser Thr Ser Gln Pro Val Thr Lys Leu Ala Thr

500

505

510

5 Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro
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15 Asn Thr Val Ser Ile Thr Glu Tyr Glu Glu Glu Ser Leu Leu Thr Ser
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20 Phe Lys Leu Asp Thr Gly Ala Glu Asp Ser Ser Gly Ser Ser Pro Ala
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25 Thr Ser Ala Ile Pro Phe Ile Ser Glu Asn Ile Ser Gln Gly Tyr Ile
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30 Phe Ser Ser Glu Asn Pro Glu Thr Ile Thr Tyr Asp Val Leu Ile Pro
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Glu Ser Ala Arg Asn Ala Ser Glu Asp Ser Thr Ser Ser Gly Ser Glu
625 630 635 640

35 Glu Ser Leu Lys Asp Pro Ser Met Glu Gly Asn Val Trp Phe Pro Ser
645 650 655

40 Ser Thr Asp Ile Thr Ala Gln Pro Asp Val Gly Ser Gly Arg Glu Ser
660 665 670

45 Phe Leu Gln Thr Asn Tyr Thr Glu Ile Arg Val Asp Glu Ser Glu Lys
675 680 685

50 Thr Thr Lys Ser Phe Ser Ala Gly Pro Val Met Ser Gln Gly Pro Ser
690 695 700

Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
705 710 715 720

55 Thr Glu Val Thr Pro His Ala Phe Thr Pro Ser Ser Arg Gln Gln Asp

725

730

735

5

Leu Val Ser Thr Val Asn Val Val Tyr Ser Gln Thr Thr Gln Pro Val
740 745 750

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Tyr Asn Gly Glu Thr Pro Leu Gln Pro Ser Tyr Ser Ser Glu Val Phe
755 760 765

15

Pro Leu Val Thr Pro Leu Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
770 775 780

Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
785 790 795 800

20

Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
805 810 815

25

Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
820 825 830

30

Arg His Leu His Thr Val Ser Gln Ile Leu Pro Gln Val Thr Ser Ala
835 840 845

Thr Glu Ser Asp Lys Val Pro Leu His Ala Ser Leu Pro Val Ala Gly
850 855 860

35

Gly Asp Leu Leu Leu Glu Pro Ser Leu Ala Gln Tyr Ser Asp Val Leu
865 870 875 880

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Ser Thr Thr His Ala Ala Ser Glu Thr Leu Glu Phe Gly Ser Glu Ser
885 890 895

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Gly Val Leu Tyr Lys Thr Leu Met Phe Ser Gln Val Glu Pro Pro Ser
900 905 910

50

Ser Asp Ala Met Met His Ala Arg Ser Ser Gly Pro Glu Pro Ser Tyr
915 920 925

Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr
930 935 940

55

Ser Ser Ala Ile Pro Val His Asp Ser Val Gly Val Thr Tyr Gln Gly

945

950

955

960

5

Ser Leu Phe Ser Gly Pro Ser His Ile Pro Ile Pro Lys Ser Ser Leu
965 970 975

10

Ile Thr Pro Thr Ala Ser Leu Leu Gln Pro Thr His Ala Leu Ser Gly
980 985 990

Asp Gly Glu Trp Ser Gly Ala Ser Ser Asp Ser Glu Phe Leu Leu Pro
995 1000 1005

15

Asp Thr Asp Gly Leu Thr Ala Leu Asn Ile Ser Ser Pro Val Ser
1010 1015 1020

20

Val Ala Glu Phe Thr Tyr Thr Thr Ser Val Phe Gly Asp Asp Asn
1025 1030 1035

25

Lys Ala Leu Ser Lys Ser Glu Ile Ile Tyr Gly Asn Glu Thr Glu
1040 1045 1050

30

Leu Gln Ile Pro Ser Phe Asn Glu Met Val Tyr Pro Ser Glu Ser
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Thr Val Met Pro Asn Met Tyr Asp Asn Val Asn Lys Leu Asn Ala
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Ser Leu Gln Glu Thr Ser Val Ser Ile Ser Ser Thr Lys Gly Met
1085 1090 1095

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Phe Pro Gly Ser Leu Ala His Thr Thr Thr Lys Val Phe Asp His
1100 1105 1110

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Glu Ile Ser Gln Val Pro Glu Asn Asn Phe Ser Val Gln Pro Thr
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His Thr Val Ser Gln Ala Ser Gly Asp Thr Ser Leu Lys Pro Val
1130 1135 1140

Leu Ser Ala Asn Ser Glu Pro Ala Ser Ser Asp Pro Ala Ser Ser
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Glu Met Leu Ser Pro Ser Thr Gln Leu Leu Phe Tyr Glu Thr Ser

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5 Ala Ser Phe Ser Thr Glu Val Leu Leu Gln Pro Ser Phe Gln Ala
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10 Ser Asp Val Asp Thr Leu Leu Lys Thr Val Leu Pro Ala Val Pro
1190 1195 1200

15 Ser Asp Pro Ile Leu Val Glu Thr Pro Lys Val Asp Lys Ile Ser
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20 Ser Thr Met Leu His Leu Ile Val Ser Asn Ser Ala Ser Ser Glu
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25 Asn Met Leu His Ser Thr Ser Val Pro Val Phe Asp Val Ser Pro
1235 1240 1245

30 Thr Ser His Met His Ser Ala Ser Leu Gln Gly Leu Thr Ile Ser
1250 1255 1260

35 Tyr Ala Ser Glu Lys Tyr Glu Pro Val Leu Leu Lys Ser Glu Ser
1265 1270 1275

40 Ser His Gln Val Val Pro Ser Leu Tyr Ser Asn Asp Glu Leu Phe
1280 1285 1290

45 Gln Thr Ala Asn Leu Glu Ile Asn Gln Ala His Pro Pro Lys Gly
1295 1300 1305

50 Arg His Val Phe Ala Thr Pro Val Leu Ser Ile Asp Glu Pro Leu
1310 1315 1320

55 Asn Thr Leu Ile Asn Lys Leu Ile His Ser Asp Glu Ile Leu Thr
1325 1330 1335

Ser Thr Lys Ser Ser Val Thr Gly Lys Val Phe Ala Gly Ile Pro
1340 1345 1350

Thr Val Ala Ser Asp Thr Phe Val Ser Thr Asp His Ser Val Pro
1355 1360 1365

Ile Gly Asn Gly His Val Ala Ile Thr Ala Val Ser Pro His Arg

1370 1375 1380

5 Asp Gly Ser Val Thr Ser Thr Lys Leu Leu Phe Pro Ser Lys Ala
1385 1390 1395

10 Thr Ser Glu Leu Ser His Ser Ala Lys Ser Asp Ala Gly Leu Val
1400 1405 1410

15 Gly Gly Gly Glu Asp Gly Asp Thr Asp Asp Asp Gly Asp Asp Asp
1415 1420 1425

20 Asp Asp Arg Asp Ser Asp Gly Leu Ser Ile His Lys Cys Met Ser
1430 1435 1440

25 Cys Ser Ser Tyr Arg Glu Ser Gln Glu Lys Val Met Asn Asp Ser
1445 1450 1455

30 Asp Thr His Glu Asn Ser Leu Met Asp Gln Asn Asn Pro Ile Ser
1460 1465 1470

35 Tyr Ser Leu Ser Glu Asn Ser Glu Glu Asp Asn Arg Val Thr Ser
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40 Val Ser Ser Asp Ser Gln Thr Gly Met Asp Arg Ser Pro Gly Lys
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55 Pro Glu Ser Lys Ala Trp Ala Val Leu Thr Ser Asp Glu Glu Ser
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60 Gly Ser Gly Gln Gly Thr Ser Asp Ser Leu Asn Glu Asn Glu Thr
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65 Ser Thr Asp Phe Ser Phe Ala Asp Thr Asn Glu Lys Asp Ala Asp
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70 Gly Ile Leu Ala Ala Gly Asp Ser Glu Ile Thr Pro Gly Phe Pro

1580 1585 1590

5 Gln Ser Pro Thr Ser Ser Val Thr Ser Glu Asn Ser Glu Val Phe
 1595 1600 1605

10 His Val Ser Glu Ala Glu Ala Ser Asn Ser Ser His Glu Ser Arg
 1610 1615 1620

15 Ile Gly Leu Ala Glu Gly Leu Glu Ser Glu Lys Lys Ala Val Ile
 1625 1630 1635

20 Pro Leu Val Ile Val Ser Ala Leu Thr Phe Ile Cys Leu Val Val
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25 Leu Val Gly Ile Leu Ile Tyr Trp Arg Lys Cys Phe Gln Thr Ala
 1655 1660 1665

30 His Phe Tyr Leu Glu Asp Ser Thr Ser Pro Arg Val Ile Ser Thr
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35 Pro Pro Thr Pro Ile Phe Pro Ile Ser Asp Asp Val Gly Ala Ile
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45 Ser Gly Phe Thr Glu Glu Phe Glu Thr Leu Lys Glu Phe Tyr Gln
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50 Glu Val Gln Ser Cys Thr Val Asp Leu Gly Ile Thr Ala Asp Ser
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55 Ser Asn His Pro Asp Asn Lys His Lys Asn Arg Tyr Ile Asn Ile
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60 Val Ala Tyr Asp His Ser Arg Val Lys Leu Ala Gln Leu Ala Glu
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70 Gly Tyr Asn Arg Pro Lys Ala Tyr Ile Ala Ala Gln Gly Pro Leu

1790 1795 1800

5 Lys Ser Thr Ala Glu Asp Phe Trp Arg Met Ile Trp Glu His Asn
1805 1810 1815

10 Val Glu Val Ile Val Met Ile Thr Asn Leu Val Glu Lys Gly Arg
1820 1825 1830

Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly Ser Glu Glu Tyr
1835 1840 1845

15 Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val Leu Ala Tyr
1850 1855 1860

20 Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile Lys Lys
1865 1870 1875

25 Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln Tyr
1880 1885 1890

30 His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu
1895 1900 1905

35 Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His
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Ala Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg
1925 1930 1935

40 Thr Gly Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln
1940 1945 1950

45 His Glu Gly Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg
1955 1960 1965

50 Ser Gln Arg Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe
1970 1975 1980

Ile His Asp Thr Leu Val Glu Ala Ile Leu Ser Lys Glu Thr Glu
1985 1990 1995

55 Val Leu Asp Ser His Ile His Ala Tyr Val Asn Ala Leu Leu Ile

2000 2005 2010

5 Pro Gly Pro Ala Gly Lys Thr Lys Leu Glu Lys Gln Phe Gln Leu
2015 2020 2025

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2030 2035 2040

15 Lys Gln Cys Asn Arg Glu Lys Asn Arg Thr Ser Ser Ile Ile Pro
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20 Val Glu Arg Ser Arg Val Gly Ile Ser Ser Leu Ser Gly Glu Gly
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30 Asn Glu Phe Ile Ile Thr Gln His Pro Leu Leu His Thr Ile Lys
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45 Trp Pro Asn Lys Asp Glu Pro Ile Asn Cys Glu Ser Phe Lys Val
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50 Thr Leu Met Ala Glu Glu His Lys Cys Leu Ser Asn Glu Glu Lys
2150 2155 2160

55 Leu Ile Ile Gln Asp Phe Ile Leu Glu Ala Thr Gln Asp Asp Tyr
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Val Leu Glu Val Arg His Phe Gln Cys Pro Lys Trp Pro Asn Pro
2180 2185 2190

Asp Ser Pro Ile Ser Lys Thr Phe Glu Leu Ile Ser Val Ile Lys
2195 2200 2205

Glu Glu Ala Ala Asn Arg Asp Gly Pro Met Ile Val His Asp Glu

2210

2215

2220

5 His Gly Gly Val Thr Ala Gly Thr Phe Cys Ala Leu Thr Thr Leu
2225 2230 2235

10 Met His Gln Leu Glu Lys Glu Asn Ser Val Asp Val Tyr Gln Val
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15 Ala Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Ala Asp Ile
2255 2260 2265

20 Glu Gln Tyr Gln Phe Leu Tyr Lys Val Ile Leu Ser Leu Val Ser
2270 2275 2280

25 Thr Arg Gln Glu Glu Asn Pro Ser Thr Ser Leu Asp Ser Asn Gly
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<223> Angiopoietin-like 2 (ANGPTL2), mRNA

<220>

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<222> (1)..(1518)

<223> Kim, I., Moon, S.O., Koh, K.N., Kim, H., Uhm, C.S., Kwak, H.J., Kim, N.G. and Koh, G.Y., "Molecular cloning, expression, and characterization of angiopoietin-related protein. angiopoietin-related protein induces endothelial cell sprouting", J. Biol. Chem. 274 (37), 26523-26528 (1999)

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Leu Gly Leu Leu Ala Ala Met Gly Ala Val Ala Gly Gln Glu Asp Gly
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Phe Glu Gly Thr Glu Glu Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn
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agg tac aag cgg gcg ggc gag tcc cag gac aag tgc acc tac acc ttc 195
Arg Tyr Lys Arg Ala Gly Glu Ser Gln Asp Lys Cys Thr Tyr Thr Phe
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att gtg ccc cag cag cgg gtc acg ggt gcc atc tgc gtc aac tcc aag 243
Ile Val Pro Gln Gln Arg Val Thr Gly Ala Ile Cys Val Asn Ser Lys
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gag cct gag gtg ctt ctg gag aac cga gtg cat aag cag gag cta gag 291
Glu Pro Glu Val Leu Leu Glu Asn Arg Val His Lys Gln Glu Leu Glu
75 80 85 90

ctg ctc aac aat gag ctg ctc aag cag aag cgg cag atc gag aca ctg 339
Leu Leu Asn Asn Glu Leu Leu Lys Gln Lys Arg Gln Ile Glu Thr Leu
95 100 105

cag cag ctg gtg gag gtg gac ggc ggc att gtg agc gag gtg aag ctg 387
Gln Gln Leu Val Glu Val Asp Gly Gly Ile Val Ser Glu Val Lys Leu
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ctg cgc aag gag agc cgc aac atg aac tcg cgg gtc acg cag ctc tac 435
Leu Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr
125 130 135

atg cag ctc ctg cac gag atc atc cgc aag cgg gac aac gcg ttg gag 483
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Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu His Lys Tyr Gln His Leu
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15 gcc aca ctg gcc cac aac caa tca gag atc atc gcg cag ctt gag gag 627
Ala Thr Leu Ala His Asn Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu
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25 gct gcc ccg ccc cgg gtc tac caa cca ccc acc tac aac cgc atc atc 723
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220 225 230

30 aac cag atc tct acc aac gag atc cag agt gac cag aac ctg aag gtg 771
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35 ctg cca ccc cct ctg ccc act atg ccc act ctc acc agc ctc cca tct 819
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255 260 265

40 tcc acc gac aag ccg tcg ggc cca tgg aga gac tgc ctg cag gcc ctg 867
Ser Thr Asp Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu
270 275 280

45 gag gat ggc cac gac acc agc tcc atc tac ctg gtg aag ccg gag aac 915
Glu Asp Gly His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn
285 290 295

50 acc aac cgc ctc atg cag gtg tgg tgc gac cag aga cac gac ccc ggg 963
Thr Asn Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly
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315 320 325 330

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335 340 345

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Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn
350 355 360

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 gca gaa tac gcc agt ttc cgc ctg gaa cct gag agc gag tat tat aag 1203
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 Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp
 395 400 405 410
 cac aac ggc aag cag ttc acc acc ctg gac aga gat cat gat gtc tac 1299
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 Thr Gly Asn Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala
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 tgt gcc cac tcc aac ctc aac ggg gtc tgg tac cgc ggg ggc cat tac 1395
 Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr
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 cgg agc cgc tac cag gac gga gtc tac tgg gct gag ttc cga gga ggc 1443
 Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly
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35 40 45

Glu Ser Gln Asp Lys Cys Thr Tyr Thr Phe Ile Val Pro Gln Gln Arg
50 55 60

Val Thr Gly Ala Ile Cys Val Asn Ser Lys Glu Pro Glu Val Leu Leu
65 70 75 80

Glu Asn Arg Val His Lys Gln Glu Leu Glu Leu Leu Asn Asn Glu Leu
85 90 95

Leu Lys Gln Lys Arg Gln Ile Glu Thr Leu Gln Gln Leu Val Glu Val
100 105 110

Asp Gly Gly Ile Val Ser Glu Val Lys Leu Leu Arg Lys Glu Ser Arg
115 120 125

Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu
130 135 140

Ile Ile Arg Lys Arg Asp Asn Ala Leu Glu Leu Ser Gln Leu Glu Asn
145 150 155 160

5 Arg Ile Leu Asn Gln Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr
165 170 175

10 Lys Asp Leu Glu His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn
180 185 190

15 Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro
195 200 205

20 Ser Ala Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val
210 215 220

25 Tyr Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
225 230 235 240

30 Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu Pro
245 250 255

35 Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys Pro Ser
260 265 270

40 Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly His Asp Thr
275 280 285

45 Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg Leu Met Gln
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50 Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln
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55 Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp Glu Thr Tyr
325 330 335

60 Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu Gly Leu Glu
340 345 350

65 Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu Leu Val Thr
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70 Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr Ala Ser Phe
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Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr
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His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe
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Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His
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Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
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Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp
450 455 460

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 Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
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 10 gca gcc cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa 153
 Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
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 15 gaa act gtg gca gag gtg act gag gta tct gtg gga gct aat cct gtc 201
 Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
 35 40 45
 20 cag gtg gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag 249
 Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
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 25 gag gtg gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc 297
 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
 65 70 75 80
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 Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
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 Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
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 Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
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 Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
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 55 acc gaa ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc 585
 Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
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 60 acc ctg tat gag agg gat gag gac aac aac ctt ctg act gag aag cag 633
 Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
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 65 aag ctg cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca 681
 Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala

195 200 205

5 gga gac cac ccc gtg gag ctg ctg gcc cgg gac ttc gag aag aac tat 729
Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Phe Glu Lys Asn Tyr
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Asn Met Tyr Ile Phe Pro Val His Trp Gln Phe Gly Gln Leu Asp Gln
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15 cac ccc att gac ggg tac ctc tcc cac acc gag ctg gct cca ctg cgt 825
His Pro Ile Asp Gly Tyr Leu Ser His Thr Glu Leu Ala Pro Leu Arg
245 250 255

20 gct ccc ctc atc ccc atg gag cat tgc acc acc cgc ttt ttc gag acc 873
Ala Pro Leu Ile Pro Met Glu His Cys Thr Thr Arg Phe Phe Glu Thr
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25 tgt gac ctg gac aat gac aag tac atc gcc ctg gat gag tgg gcc ggc 921
Cys Asp Leu Asp Asn Asp Lys Tyr Ile Ala Leu Asp Glu Trp Ala Gly
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30 tgc ttc ggc atc aag cag aag gat atc gac aag gat ctt gtg atc taa 969
Cys Phe Gly Ile Lys Gln Lys Asp Ile Asp Lys Asp Leu Val Ile
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Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
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Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
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Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
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Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
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Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
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Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
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Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
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Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
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Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
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Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
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Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
195 200 205

Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Phe Glu Lys Asn Tyr
210 215 220

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Asn Met Tyr Ile Phe Pro Val His Trp Gln Phe Gly Gln Leu Asp Gln
225 230 235 240

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His Pro Ile Asp Gly Tyr Leu Ser His Thr Glu Leu Ala Pro Leu Arg
245 250 255

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Ala Pro Leu Ile Pro Met Glu His Cys Thr Thr Arg Phe Phe Glu Thr
260 265 270

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Cys Asp Leu Asp Asn Asp Lys Tyr Ile Ala Leu Asp Glu Trp Ala Gly
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Cys Phe Gly Ile Lys Gln Lys Asp Ile Asp Lys Asp Leu Val Ile
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<223> Park,M., Dean,M., Kaul,K., Braun,M.J., Gonda,M.A. and Vande Woude
,G. TITLE Sequence of MET protooncogene cDNA has features charact
eristic of the tyrosine kinase family of growth-factor receptors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (18), 6379-6383 (1987)

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ataaacctct cata atg aag gcc ccc gct gtg ctt gca cct ggc atc ctc 230
Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu
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gtg ctc ctg ttt acc ttg gtg cag agg agc aat ggg gag tgt aaa gag 278
Val Leu Leu Phe Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu
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gca cta gca aag tcc gag atg aat gtg aat atg aag tat cag ctt ccc 326
Ala Leu Ala Lys Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro
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aac ttc acc gcg gaa aca ccc atc cag aat gtc att cta cat gag cat 374
Asn Phe Thr Ala Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His
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cac att ttc ctt ggt gcc act aac tac att tat gtt tta aat gag gaa 422
His Ile Phe Leu Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu
65 70 75

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gac ctt cag aag gtt gct gag tac aag act ggg cct gtg ctg gaa cac 470
Asp Leu Gln Lys Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His
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cca gat tgt ttc cca tgt cag gac tgc agc agc aaa gcc aat tta tca 518
Pro Asp Cys Phe Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser
95 100 105

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gga ggt gtt tgg aaa gat aac atc aac atg gct cta gtt gtc gac acc 566
Gly Gly Val Trp Lys Asp Asn Ile Asn Met Ala Leu Val Val Asp Thr
110 115 120

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tac tat gat gat caa ctc att agc tgt ggc agc gtc aac aga ggg acc 614
Tyr Tyr Asp Asp Gln Leu Ile Ser Cys Gly Ser Val Asn Arg Gly Thr
125 130 135 140

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	Glu	Val	His	Cys	Ile	Phe	Ser	Pro	Gln	Ile	Glu	Glu	Pro	Ser	Gln	Cys	
				160					165					170			
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	Pro	Asp	Cys	Val	Val	Ser	Ala	Leu	Gly	Ala	Lys	Val	Leu	Ser	Ser	Val	
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15	aag	gac	cgg	ttc	atc	aac	ttc	ttt	gta	ggc	aat	acc	ata	aat	tct	tct	806
	Lys	Asp	Arg	Phe	Ile	Asn	Phe	Phe	Val	Gly	Asn	Thr	Ile	Asn	Ser	Ser	
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	Tyr	Phe	Pro	Asp	His	Pro	Leu	His	Ser	Ile	Ser	Val	Arg	Arg	Leu	Lys	
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25	gaa	acg	aaa	gat	ggt	ttt	atg	ttt	ttg	acg	gac	cag	tcc	tac	att	gat	902
	Glu	Thr	Lys	Asp	Gly	Phe	Met	Phe	Leu	Thr	Asp	Gln	Ser	Tyr	Ile	Asp	
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	Val	Leu	Pro	Glu	Phe	Arg	Asp	Ser	Tyr	Pro	Ile	Lys	Tyr	Val	His	Ala	
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	Phe	Glu	Ser	Asn	Asn	Phe	Ile	Tyr	Phe	Leu	Thr	Val	Gln	Arg	Glu	Thr	
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40	cta	gat	gct	cag	act	ttt	cac	aca	aga	ata	atc	agg	ttc	tgt	tcc	ata	1046
	Leu	Asp	Ala	Gln	Thr	Phe	His	Thr	Arg	Ile	Ile	Arg	Phe	Cys	Ser	Ile	
				270			275					280					
45	aac	tct	gga	ttg	cat	tcc	tac	atg	gaa	atg	cct	ctg	gag	tgt	att	ctc	1094
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	Thr	Glu	Lys	Arg	Lys	Lys	Arg	Ser	Thr	Lys	Lys	Glu	Val	Phe	Asn	Ile	
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	Leu	Gln	Ala	Ala	Tyr	Val	Ser	Lys	Pro	Gly	Ala	Gln	Leu	Ala	Arg	Gln	
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	Ile	Gly	Ala	Ser	Leu	Asn	Asp	Asp	Ile	Leu	Phe	Gly	Val	Phe	Ala	Gln	
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	Ser	Lys	Pro	Asp	Ser	Ala	Glu	Pro	Met	Asp	Arg	Ser	Ala	Met	Cys	Ala	
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	Arg	Asp	Glu	Tyr	Arg	Thr	Glu	Phe	Thr	Thr	Ala	Leu	Gln	Arg	Val	Asp	
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	Arg	Phe	Met	Gln	Val	Val	Ser	Arg	Ser	Gly	Pro	Ser	Thr	Pro	His		
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	Glu	His	Thr	Leu	Asn	Gln	Asn	Gly	Tyr	Thr	Leu	Val	Ile	Thr	Gly	Lys	
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 Ser Tyr Val Asp Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro
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 Pro Thr Lys Ser Phe Ile Ser Gly Gly Ser Thr Ile Thr Gly Val Gly
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 Lys Asn Leu Asn Ser Val Ser Val Pro Arg Met Val Ile Asn Val His
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 Glu Ile Ile Cys Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln
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Leu Pro Leu Lys Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser
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5 aaa tac ttt gat ctc att tat gta cat aat cct gtg ttt aag cct ttt 2726
Lys Tyr Phe Asp Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe
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Val Gly Asn Lys Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val
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Val His Val Asn Ala Thr Tyr Val Asn Val Lys Cys Val Ala Pro
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Tyr Pro Ser Leu Leu Ser Ser Glu Asp Asn Ala Asp Asp Glu Val
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Asp Thr Arg Pro Ala Ser Phe Trp Glu Thr Ser
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Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys
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Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala
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Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
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Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu Glu Asp Leu Gln Lys
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Val Ala Glu Tyr Lys Thr Gly Pro Val Leu Glu His Pro Asp Cys Phe
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Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
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 70 Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser
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5 Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys
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Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
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30 Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu Trp Lys
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Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln Pro Asp
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40 Leu Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg Lys Gln
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50 Thr Pro His Leu Asp Arg Leu Val Ser Ala Arg Ser Val Ser Pro Thr
980 985 990

55 Thr Glu Met Val Ser Asn Glu Ser Val Asp Tyr Arg Ala Thr Phe Pro
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Glu Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg Gln
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 Tyr Met Lys His Gly Asp Leu Arg Asn Phe Ile Arg Asn Glu Thr
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<222> (1)..(2558)

20 <223> Gary,S.C., Zerillo,C.A., Chiang,V.L., Gaw,J.U., Gray,G. and Hockf
ield,S. TITLE cDNA cloning, chromosomal localization, and express
ion analysis of human BEHAB/brevican, a brain specific proteoglyc
an regulated during cortical development and in glioma JOURNAL Ge
ne 256 (1-2), 139-147 (2000)

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55	gca ttg gag gaa gaa gag aaa tat gaa gat gaa gaa gag aaa gag gag Ala Leu Glu Glu Glu Glu Lys Tyr Glu Asp Glu Glu Glu Lys Glu Glu 455 460 465			1448
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Gln Pro Gly Ala Ser Pro Leu Pro Asp Gly Glu Ser Glu Ala Ser Arg
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Pro Pro Arg Val His Gly Pro Pro Thr Glu Thr Leu Pro Thr Pro Arg
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Glu Arg Asn Leu Ala Ser Pro Ser Pro Ser Thr Leu Val Glu Ala Arg
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Gly Glu Ser Glu Glu Thr Gly Ser Ser Glu Gly Ala Pro Ser Leu Leu
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Pro Ala Thr Arg Ala Pro Glu Gly Thr Arg Glu Leu Glu Ala Pro Ser
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Gln Pro Val Leu Pro Thr Asp Ser Ala Ser Arg Gly Gly Val Ala Val
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Arg Ala Phe Arg Val Arg Ile Ala Gly Asp Ala Pro Leu Gln Gly Val
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Leu Gly Gly Ala Leu Thr Ile Pro Cys His Val His Tyr Leu Arg Pro
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Pro Pro Ser Arg Arg Ala Val Leu Gly Ser Pro Arg Val Lys Trp Thr
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Phe Leu Ser Arg Gly Arg Glu Ala Glu Val Leu Val Ala Arg Gly Val
85 90 95

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Arg Val Lys Val Asn Glu Ala Tyr Arg Phe Arg Val Ala Leu Pro Ala
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Tyr Pro Ala Ser Leu Thr Asp Val Ser Leu Ala Leu Ser Glu Leu Arg

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5 Pro Asn Asp Ser Gly Ile Tyr Arg Cys Glu Val Gln His Gly Ile Asp
130 135 140

10 Asp Ser Ser Asp Ala Val Glu Val Lys Val Lys Gly Val Val Phe Leu
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15 Tyr Arg Glu Gly Ser Ala Arg Tyr Ala Phe Ser Phe Ser Gly Ala Gln
165 170 175

20 Glu Ala Cys Ala Arg Ile Gly Ala His Ile Ala Thr Pro Glu Gln Leu
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25 Tyr Ala Ala Tyr Leu Gly Gly Tyr Glu Gln Cys Asp Ala Gly Trp Leu
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30 Ser Asp Gln Thr Val Arg Tyr Pro Ile Gln Thr Pro Arg Glu Ala Cys
210 215 220

35 Tyr Gly Asp Met Asp Gly Phe Pro Gly Val Arg Asn Tyr Gly Val Val
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45 Gly Glu Leu Phe Leu Gly Asp Pro Pro Glu Lys Leu Thr Leu Glu Glu
260 265 270

50 Ala Arg Ala Tyr Cys Gln Glu Arg Gly Ala Glu Ile Ala Thr Thr Gly
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290 295 300

60 Trp Leu Ala Asp Gly Ser Val Arg Tyr Pro Ile Val Thr Pro Ser Gln
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65 Arg Cys Gly Gly Gly Leu Pro Gly Val Lys Thr Leu Phe Leu Phe Pro
325 330 335

70 Asn Gln Thr Gly Phe Pro Asn Lys His Ser Arg Phe Asn Val Tyr Cys

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345

350

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Phe Arg Asp Ser Ala Gln Pro Ser Ala Ile Pro Glu Ala Ser Asn Pro
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Ala Ser Asn Pro Ala Ser Asp Gly Leu Glu Ala Ile Val Thr Val Thr
370 375 380

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Glu Thr Leu Glu Glu Leu Gln Leu Pro Gln Glu Ala Thr Glu Ser Glu
385 390 395 400

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Ser Arg Gly Ala Ile Tyr Ser Ile Pro Ile Met Glu Asp Gly Gly Gly
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Gly Ser Ser Thr Pro Glu Asp Pro Ala Glu Ala Pro Arg Thr Leu Leu
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Glu Phe Glu Thr Gln Ser Met Val Pro Pro Thr Gly Phe Ser Glu Glu
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Glu Gly Lys Ala Leu Glu Glu Glu Glu Lys Tyr Glu Asp Glu Glu Glu
450 455 460

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Lys Glu Glu Glu Glu Glu Glu Glu Glu Val Glu Asp Glu Ala Leu Trp
465 470 475 480

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Ala Trp Pro Ser Glu Leu Ser Ser Pro Gly Pro Glu Ala Ser Leu Pro
485 490 495

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Thr Glu Pro Ala Ala Gln Glu Glu Ser Leu Ser Gln Ala Pro Ala Arg
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Ala Val Leu Gln Pro Gly Ala Ser Pro Leu Pro Asp Gly Glu Ser Glu
515 520 525

Ala Ser Arg Pro Pro Arg Val His Gly Pro Pro Thr Glu Thr Leu Pro
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Thr Pro Arg Glu Arg Asn Leu Ala Ser Pro Ser Pro Ser Thr Leu Val
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Glu Ala Arg Glu Val Gly Glu Ala Thr Gly Gly Pro Glu Leu Ser Gly

565

570

575

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Val Pro Arg Gly Glu Ser Glu Glu Thr Gly Ser Ser Glu Gly Ala Pro
580 585 590

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Ser Leu Leu Pro Ala Thr Arg Ala Pro Glu Gly Thr Arg Glu Leu Glu
595 600 605

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Ala Pro Ser Glu Asp Asn Ser Gly Arg Thr Ala Pro Ala Gly Thr Ser
610 615 620

Val Gln Ala Gln Pro Val Leu Pro Thr Asp Ser Ala Ser Arg Gly Gly
625 630 635 640

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Val Ala Val Val Pro Ala Ser Gly Asn Ser Ala Gln Gly Ser Thr Ala
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Leu Ser Ile Leu Leu Leu Phe Phe Pro Leu Gln Leu Trp Val Thr
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<221> REFERENCE

<222> (1) .. (2316)

55

<223> Stamenkovic, I., Aruffo, A., Amiot, M. and Seed, B. TITLE The hematopoietic and epithelial forms of CD44 are distinct polypeptides with different adhesion potentials for hyaluronate-bearing cells JOU

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20 acc atg gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg 168
Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val
1 5 10 15
25 ccg ctg agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca 216
Pro Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala
20 25 30
30 ggt gta ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg 264
Gly Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr
35 40 45
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Glu Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met
50 55 60
40 gcc cag atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat 360
Ala Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr
65 70 75
45 ggg ttc ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc 408
Gly Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser
80 85 90 95
50 atc tgt gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc 456
Ile Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr
100 105 110
55 tcc cag tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa 504
Ser Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu
115 120 125
gat tgt aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att 552
Asp Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile
130 135 140
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Thr Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly
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Glu Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp
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10 gat gac gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga 696
Asp Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly
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15 ggt tac atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa 744
Gly Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu
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gac agt ccc tgg atc acc gac agc aca gac aga atc cct cgt acc aat 792
Asp Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Arg Thr Asn
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Met Asp Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn
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25 aca ggt ttg gtg gaa gat ttg gac agg aca gga cct ctt tca atg aca 888
Thr Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr
240 245 250 255

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Thr Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu
260 265 270

gaa gaa gat aaa gac cat cca aca act tct act ctg aca tca agc aat 984
Glu Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn
275 280 285

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Arg Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly
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Ser Thr His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys
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Glu Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe
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Ser Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His
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Gly Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro
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Glu Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu
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Ala Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys
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Ser Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu
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Val Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp
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65 aacctaccac atagttattc ctgatcgcca accttgcccc ccaccagcta aggacatttc 1965

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90 gtccttttat tcagtataat tttttaagT tactttgtca gaggcacaaa aagggtttta 2265

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N 7)

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Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
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Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
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Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser
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Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
130 135 140

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
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Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
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Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
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Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
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Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Thr Leu
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Met Ser Thr Ser Ala Thr Ala Thr Glu Thr Ala Thr Lys Arg Gln Glu
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Thr Trp Asp Trp Phe Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn
245 250 255

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His Leu His Thr Thr Thr Gln Met Ala Gly Thr Ser Ser Asn Thr Ile
260 265 270

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Ser Ala Gly Trp Glu Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg
275 280 285

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His Leu Ser Phe Ser Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile
290 295 300

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Ser Ser Thr Ile Ser Thr Thr Pro Arg Ala Phe Asp His Thr Lys Gln
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Asn Gln Asp Trp Thr Gln Trp Asn Pro Ser His Ser Asn Pro Glu Val
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Leu Leu Gln Thr Thr Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr
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Thr Ala Tyr Glu Gly Asn Trp Asn Pro Glu Ala His Pro Pro Leu Ile
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His His Glu His His Glu Glu Glu Glu Thr Pro His Ser Thr Ser Thr
370 375 380

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Ile Gln Ala Thr Pro Ser Ser Thr Thr Glu Glu Thr Ala Thr Gln Lys
385 390 395 400

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Glu Gln Trp Phe Gly Asn Arg Trp His Glu Gly Tyr Arg Gln Thr Pro
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Arg Glu Asp Ser His Ser Thr Thr Gly Thr Ala Ala Ala Ser Ala His
420 425 430

Thr Ser His Pro Met Gln Gly Arg Thr Thr Pro Ser Pro Glu Asp Ser
435 440 445

Ser Trp Thr Asp Phe Phe Asn Pro Ile Ser His Pro Met Gly Arg Gly
450 455 460

His Gln Ala Gly Arg Arg Met Asp Met Asp Ser Ser His Ser Thr Thr
465 470 475 480

Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly Leu Val Glu Asp Leu Asp
485 490 495

Arg Thr Gly Pro Leu Ser Met Thr Thr Gln Gln Ser Asn Ser Gln Ser
500 505 510

Phe Ser Thr Ser His Glu Gly Leu Glu Glu Asp Lys Asp His Pro Thr
515 520 525

Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn Asp Val Thr Gly Gly Arg
530 535 540

Arg Asp Pro Asn His Ser Glu Gly Ser Thr Thr Leu Leu Glu Gly Tyr
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Thr Ser His Tyr Pro His Thr Lys Glu Ser Arg Thr Phe Ile Pro Val
565 570 575

Thr Ser Ala Lys Thr Gly Ser Phe Gly Val Thr Ala Val Thr Val Gly
580 585 590

Asp Ser Asn Ser Asn Val Asn Arg Ser Leu Ser Gly Asp Gln Asp Thr
595 600 605

Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu Ser Asp
610 615 620

Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr Ser Gly
625 630 635 640

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Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu Ala Ser
645 650 655

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Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser
660 665 670

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Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser Gly Asn
675 680 685

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Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu Ala Ser
690 695 700

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Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser Glu Thr
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<223> Todd, S.C., Doctor, V.S. and Levy, S. TITLE Sequences and express
ion of six new members of the tetraspanin/TM4SF family JOURNAL Bi
ochim. Biophys. Acta 1399 (1), 101-104 (1998)

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aac ctc atc ttc tgg ggg gca gct ggc att tta tgc tat gtg gga gcc	96
Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala	
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tat gtc ttc atc act tat gat gac tat gac cac ttc ttt gaa gat gtg	144
Tyr Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val	
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tac acg ctc atc cct gct gta gtg atc ata gct gta gga gcc ctg ctt	192
Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Gly Ala Leu Leu	
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ttc atc att ggg cta att ggc tgc tgt gcc aca atc cgg gaa agt cgc	240
Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg	
65 70 75 80	

tgt gga ctt gcc acg ttt gtc atc atc ctg ctc ttg gtt ttt gtc aca	288
Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr	
85 90 95	

gaa gtt gtt gta gtg gtt ttg gga tat gtt tac aga gca aag gtg gaa	336
Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu	
100 105 110	

aat gag gtt gat cgc agc att cag aaa gtg tat aag acc tac aat gga	384
Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys Thr Tyr Asn Gly	
115 120 125	

acc aac cct gat gct gct agc cgg gct att gat tat gta cag aga cag	432
Thr Asn Pro Asp Ala Ala Ser Arg Ala Ile Asp Tyr Val Gln Arg Gln	
130 135 140	

ctg cat tgt tgt gga att cac aac tac tca gac tgg gaa aat aca gat 480
Leu His Cys Cys Gly Ile His Asn Tyr Ser Asp Trp Glu Asn Thr Asp
145 150 155 160

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Trp Phe Lys Glu Thr Lys Asn Gln Ser Val Pro Leu Ser Cys Cys Arg
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Glu Thr Ala Ser Asn Cys Asn Gly Ser Leu Ala His Pro Ser Asp Leu
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Tyr Ala Glu Gly Cys Glu Ala Leu Val Val Lys Lys Leu Gln Glu Ile
195 200 205

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Met Met His Val Ile Trp Ala Ala Leu Ala Phe Ala Ala Ile Gln Leu
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Leu Gly Met Leu Cys Ala Cys Ile Val Leu Cys Arg Arg Ser Arg Asp
225 230 235 240

30 cct gct tac gag ctc ctc atc act ggc gga acc tat gca tag 762
Pro Ala Tyr Glu Leu Leu Ile Thr Gly Gly Thr Tyr Ala
245 250

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40 tctgctgctg ttggcctctg gagttcattt agttaagca catgtacact ggtgttggac 882

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Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Gly Ala Leu Leu
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Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg
65 70 75 80

Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr
85 90 95

Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu
100 105 110

Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys Thr Tyr Asn Gly
115 120 125

Thr Asn Pro Asp Ala Ala Ser Arg Ala Ile Asp Tyr Val Gln Arg Gln
130 135 140

Leu His Cys Cys Gly Ile His Asn Tyr Ser Asp Trp Glu Asn Thr Asp

145 150 155 160

5 Trp Phe Lys Glu Thr Lys Asn Gln Ser Val Pro Leu Ser Cys Cys Arg
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10 Glu Thr Ala Ser Asn Cys Asn Gly Ser Leu Ala His Pro Ser Asp Leu
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15 Tyr Ala Glu Gly Cys Glu Ala Leu Val Val Lys Lys Leu Gln Glu Ile
 195 200 205

20 Met Met His Val Ile Trp Ala Ala Leu Ala Phe Ala Ala Ile Gln Leu
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<222> (1) .. (1317)

<223> Svoboda, M., Tastenoy, M., Van Rampelbergh, J., Goossens, J.F., D
e Neef, P., Waelbroeck, M. and Robberecht, P. TITLE Molecular clo
ning and functional characterization of a human VIP receptor from
SUP-T1 lymphoblasts JOURNAL Biochem. Biophys. Res. Commun. 205 (3), 1617-1624 (1994)

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<222> (1) .. (1317)

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ccc	gtg	aac	agc	att	cac	cca	gaa	tgc	cga	ttt	cat	ctg	gaa	ata	cag	96
Pro	Val	Asn	Ser	Ile	His	Pro	Glu	Cys	Arg	Phe	His	Leu	Glu	Ile	Gln	
		20					25					30				

gag	gaa	gaa	aca	aaa	tgt	aca	gag	ctt	ctg	agg	tct	caa	aca	gaa	aaa	144
Glu	Glu	Glu	Thr	Lys	Cys	Thr	Glu	Leu	Leu	Arg	Ser	Gln	Thr	Glu	Lys	
	35						40					45				

cac	aaa	gcc	tgc	agt	ggc	gtc	tgg	gac	aac	atc	acg	tgc	tgg	cgg	cct	192
His	Lys	Ala	Cys	Ser	Gly	Val	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Arg	Pro	
	50					55					60					

gcc	aat	gtg	gga	gag	acc	gtc	acg	gtg	ccc	tgc	cca	aaa	gtc	ttc	agc	240
Ala	Asn	Val	Gly	Glu	Thr	Val	Thr	Val	Pro	Cys	Pro	Lys	Val	Phe	Ser	
65					70				75					80		

aat	ttt	tac	agc	aaa	gca	gga	aac	ata	agc	aaa	aac	tgt	acg	agt	gac	288
Asn	Phe	Tyr	Ser	Lys	Ala	Gly	Asn	Ile	Ser	Lys	Asn	Cys	Thr	Ser	Asp	
			85					90						95		

gga	tgg	tca	gag	acg	ttc	cca	gat	ttc	gtc	gat	gcc	tgt	ggc	tac	agc	336
Gly	Trp	Ser	Glu	Thr	Phe	Pro	Asp	Phe	Val	Asp	Ala	Cys	Gly	Tyr	Ser	
		100						105					110			

gac	cgg	gag	gat	gag	agc	aag	atc	acg	ttt	tat	att	ctg	gtg	aag	gcc	384
Asp	Pro	Glu	Asp	Glu	Ser	Lys	Ile	Thr	Phe	Tyr	Ile	Leu	Val	Lys	Ala	
		115					120					125				

att	tat	acc	ctg	ggc	tac	agt	gtc	tct	ctg	atg	tct	ctt	gca	aca	gga	432
Ile	Tyr	Thr	Leu	Gly	Tyr	Ser	Val	Ser	Leu	Met	Ser	Leu	Ala	Thr	Gly	
	130					135					140					

agc	ata	att	ctg	tgc	ctc	ttc	agg	aag	ctg	cac	tgc	acc	agg	aat	tac	480
Ser	Ile	Ile	Leu	Cys	Leu	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Tyr	
145					150					155					160	

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	Ile His Leu Asn Leu Phe Leu Ser Phe Ile Leu Arg Ala Ile Ser Val	
	165 170 175	
5	ctg gtc aag gac gac gtt ctc tac tcc agc tct ggc acg ttg cac tgc	576
	Leu Val Lys Asp Asp Val Leu Tyr Ser Ser Ser Gly Thr Leu His Cys	
	180 185 190	
10	cct gac cag cca tcc tcc tgg gtg ggc tgc aag ctg agc ctg gtc ttc	624
	Pro Asp Gln Pro Ser Ser Trp Val Gly Cys Lys Leu Ser Leu Val Phe	
	195 200 205	
15	ctg cag tac tgc atc atg gcc aac ttc ttc tgg ctg ctg gtg gag ggg	672
	Leu Gln Tyr Cys Ile Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly	
	210 215 220	
20	ctc tac ctc cac acc ctc ctg gtg gcc atg ctc ccc cct aga agg tgc	720
	Leu Tyr Leu His Thr Leu Leu Val Ala Met Leu Pro Pro Arg Arg Cys	
	225 230 235 240	
25	ttc ctg gcc tac ctc ctg atc gga tgg ggc ctc ccc acc gtc tgc atc	768
	Phe Leu Ala Tyr Leu Leu Ile Gly Trp Gly Leu Pro Thr Val Cys Ile	
	245 250 255	
30	ggt gca tgg act gcg gcc agg ctc tac tta gaa gac acc ggt tgc tgg	816
	Gly Ala Trp Thr Ala Ala Arg Leu Tyr Leu Glu Asp Thr Gly Cys Trp	
	260 265 270	
35	gat aca aac gac cac agt gtg ccc tgg tgg gtc ata cga ata ccg att	864
	Asp Thr Asn Asp His Ser Val Pro Trp Trp Val Ile Arg Ile Pro Ile	
	275 280 285	
40	tta att tcc atc atc gtc aat ttt gtc ctt ttc att agt att ata cga	912
	Leu Ile Ser Ile Ile Val Asn Phe Val Leu Phe Ile Ser Ile Ile Arg	
	290 295 300	
45	att ttg ctg cag aag tta aca tcc cca gat gtc ggc ggc aac gac cag	960
	Ile Leu Leu Gln Lys Leu Thr Ser Pro Asp Val Gly Gly Asn Asp Gln	
	305 310 315 320	
50	tct cag tac aag agg ctg gcc aag tcc acg ctc ctg ctt atc ccg ctg	1008
	Ser Gln Tyr Lys Arg Leu Ala Lys Ser Thr Leu Leu Leu Ile Pro Leu	
	325 330 335	
55	ttc ggc gtc cac tac atg gtg ttt gcc gtg ttt ccc atc agc atc tcc	1056
	Phe Gly Val His Tyr Met Val Phe Ala Val Phe Pro Ile Ser Ile Ser	
	340 345 350	
60	tcc aaa tac cag ata ctg ttt gag ctg tgc ctc ggc tgc ttc cag ggc	1104
	Ser Lys Tyr Gln Ile Leu Phe Glu Leu Cys Leu Gly Ser Phe Gln Gly	
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65	ctg gtg gtg gcc gtc ctc tac tgt ttc ctg aac agt gag gtg cag tgc	1152
	Leu Val Val Ala Val Leu Tyr Cys Phe Leu Asn Ser Glu Val Gln Cys	
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Glu Leu Lys Arg Lys Trp Arg Ser Arg Cys Pro Thr Pro Ser Ala Ser
385 390 395 400

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Arg Asp Tyr Arg Val Cys Gly Ser Ser Phe Ser His Asn Gly Ser Glu
405 410 415

10 ggc gcc ctg cag ttc cac cgc gcg tcc cga gcc cag tcc ttc ctg caa 1296
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Glu Glu Glu Thr Lys Cys Ala Glu Leu Leu Arg Ser Gln Thr Glu Lys
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His Lys Ala Cys Ser Gly Val Trp Asp Asn Ile Thr Cys Trp Arg Pro
50 55 60

Ala Asn Val Gly Glu Thr Val Thr Val Pro Cys Pro Lys Val Phe Ser
65 70 75 80

Asn Phe Tyr Ser Lys Ala Gly Asn Ile Ser Lys Asn Cys Thr Ser Asp
85 90 95

Gly Trp Ser Glu Thr Phe Pro Asp Phe Val Asp Ala Cys Gly Tyr Ser
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115 120 125

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130 135 140

Ser Ile Ile Leu Cys Leu Phe Arg Lys Leu His Cys Thr Arg Asn Tyr
145 150 155 160

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 10 Leu Val Lys Asp Asp Val Leu Tyr Ser Ser Ser Gly Thr Leu His Cys
 180 185 190
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 195 200 205
 20 Leu Gln Tyr Cys Ile Met Ala Asn Phe Phe Trp Leu Leu Val Glu Gly
 210 215 220
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 225 230 235 240
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 245 250 255
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 260 265 270
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 275 280 285
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 65 Ser Lys Tyr Gln Ile Leu Phe Glu Leu Cys Leu Gly Ser Phe Gln Gly
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Glu Leu Lys Arg Lys Trp Arg Ser Arg Cys Pro Thr Pro Ser Ala Ser
385 390 395 400

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<222> (1) .. (889)

<223> Li, Y.S., Milner, P.G., Chauhan, A.K., Watson, M.A., Hoffman, R.M
., Kodner, C.M., Milbrandt, J. and Deuel, T.F. TITLE Cloning and
expression of a developmentally regulated protein that induces mi
togenic and neurite outgrowth activity JOURNAL Science 250 (4988)
, 1690-1694 (1990)

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gca gct gcc ttc ttg gca ttc att ttc ata ctg gca gct gtg gat act 338
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gct gaa gca ggg aag aaa gag aaa cca gaa aaa aaa gtg aag aag tct 386
Ala Glu Ala Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser
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gac tgt gga gaa tgg cag tgg agt gtg tgt gtg ccc acc agt gga gac 434
Asp Cys Gly Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp
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tgt ggg ctg ggc aca cgg gag ggc act cgg act gga gct gag tgc aag 482
Cys Gly Leu Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys
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caa acc atg aag acc cag aga tgt aag atc ccc tgc aac tgg aag aag 530
Gln Thr Met Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys
80 85 90
caa ttt ggc gcg gag tgc aaa tac cag ttc cag gcc tgg gga gaa tgt 578
Gln Phe Gly Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys
95 100 105
gac ctg aac aca gcc ctg aag acc aga act gga agt ctg aag cga gcc 626
Asp Leu Asn Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala
110 115 120 125
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Leu His Asn Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys
130 135 140
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Gly Lys Leu Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys
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Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu
50 55 60

5
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met
65 70 75 80

10
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly
85 90 95

15
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
100 105 110

20
Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
115 120 125

25
Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
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Lys Lys Gln Glu Lys Met Leu Asp
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<222> (1)..(3143)

<223> Crosby, A.H., Edwards, S.J., Murray, J.C. and Dixon, M.J. TITLE G
enomic organization of the human osteopontin gene: exclusion of t
he locus from a causative role in the pathogenesis of dentinogene
sis imperfecta type II JOURNAL Genomics 27 (1), 155-160 (1995)

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35 <222> (884) . . (964)

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gtcagcagca gcaggaggag gcagagacag catcgtcggg accagactcg tctcaggcca 180

gttgcagcct tctcagccaa acgccgacca aggtacagct tcagtttgct actgggttgt 240

gcattcagct gaatttcatg ggggaagtcca aattctaagg aaaaaaatgt ggtagtataa 300

aaaggtatca ctgttgtaac ctatgaagat gtcagctatt cctttgaaat attttgcagg 360

aaaactcact acc atg aga att gca gtg att tgc ttt tgc ctc cta ggc 409
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly
1 5 10

atc acc tgt gcc ata cca gtgagtacag ttgcatctta aagaaaattc 457
Ile Thr Cys Ala Ile Pro
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ctgaaaataa ctgaattgtg tgcttccatg tgctaggagg acattcttgt aatctttctt 517

catcttttct gtttctaag gtt aaa cag gct gat tct gga agt tct gag gaa 569
Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu
20 25

aag cag gtaagcatct tttatgtttt tatatagtta aatcatttac tcaattatgg 625
Lys Gln
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cgagaggtgc aagaaacgta tttgctgcga tcaaagtgt tcatatttgt aaagcaattt 685

gaaagagtgc ctagcccaca gtaagtgcta cataagagtt tgtaaataa atctgcaaaa 745

aaaaaaaaaa ttacaaaaag gtacctaagg gtccgggtga ctatatgctt ccatcaagac 805

tagtgaagaa tgggtgtttt ttccattcat ccctacattt ctttttttaa taatgataaa 865

catgcaactt tttttagt ctt tac aac aaa tac cca gat gct gtg gcc aca 916
Leu Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr
35 40

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Asn Ala Val Ser Ser Glu Glu Thr Asn
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Asp Phe Lys Gln Glu
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tgaaactaaa taaaaagaaa gatagtaaaa gactaatgtg ctataaaggc taagggaataa 1553
taaaaaccca tatattaatt ttcccggcca tcttaatttt cag acc ctt cca agt 1608
Thr Leu Pro Ser
75

aag tcc aac gaa agc cat gac cac atg gat gat atg gat gat gaa gat 1656
Lys Ser Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp
80 85 90

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Asp Asp Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser
95 100 105

gat gat gta gat gac act gat gat tct cac cag tct gat gag tct cac 1752
Asp Asp Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His
110 115 120

cat tct gat gaa tct gat gaa ctg gtc act gat ttt ccc acg gac ctg 1800
His Ser Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu
125 130 135 140

cca gca acc gaa gtt ttc act cca gtt gtc ccc aca gta gac aca tat 1848
Pro Ala Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr
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gat ggc cga ggt gat agt gtg gtt tat gga ctg agg tca aaa tct aag 1896
Asp Gly Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys
160 165 170

5
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aag ttt cgc aga cct gac atc cag gtaaattcctt taacagacac acctgatggt 1950
Lys Phe Arg Arg Pro Asp Ile Gln
175 180

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Tyr

cct gat gct aca gac gag gac atc acc tca cac atg gaa agc gag gag 2355
Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser Glu Glu
185 190 195

ttg aat ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg aac gcg 2403
Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu Asn Ala
200 205 210

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Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr Ser Gln
215 220 225

ctg gat gac cag agt gct gaa acc cac agc cac aag cag tcc aga tta 2499
Leu Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser Arg Leu
230 235 240 245

tat aag cgg aaa gcc aat gat gag agc aat gag cat tcc gat gtg att 2547
Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp Val Ile
250 255 260

gat agt cag gaa ctt tcc aaa gtc agc cgt gaa ttc cac agc cat gaa 2595
Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser His Glu
265 270 275

ttt cac agc cat gaa gat atg ctg gtt gta gac ccc aaa agt aag gaa 2643
Phe His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser Lys Glu
280 285 290

gaa gat aaa cac ctg aaa ttt cgt att tct cat gaa tta gat agt gca 2691
Glu Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp Ser Ala
295 300 305

tct tct gag gtc aat taa aaggagaaaa aatacaattt ctcactttgc 2739
Ser Ser Glu Val Asn
310

atttagtcaa aagaaaaaat gctttatagc aaaatgaaag agaacatgaa atgcttcttt 2799

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35 40 45

10 Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu
50 55 60

15 Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu
65 70 75 80

20 Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His
85 90 95

25 Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp
100 105 110

30 Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu
115 120 125

35 Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu
130 135 140

40 Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly
145 150 155 160

45 Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg
165 170 175

50 Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His
180 185 190

55 Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala
195 200 205

60 Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser
210 215 220

65 Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His
225 230 235 240

70 Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu
245 250 255

His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu
260 265 270

Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp
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Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His
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Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
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<222> (1)..(259)

<223> Carbonic Anhydrase domain of human carbonic anhydrase III

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His Thr Lys Asp Ile Arg His Asp Pro Ser Leu Gln Pro Trp Ser Val
35 40 45

Ser Tyr Asp Gly Gly Ser Ala Lys Thr Ile Leu Asn Asn Gly Lys Thr
50 55 60

5 Cys Arg Val Val Phe Asp Asp Thr Tyr Asp Arg Ser Met Leu Arg Gly
65 70 75 80

10 Gly Pro Leu Pro Gly Pro Tyr Arg Leu Arg Gln Phe His Leu His Trp
85 90 95

15 Gly Ser Ser Asp Asp His Gly Ser Glu His Thr Val Asp Gly Val Lys
100 105 110

20 Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Pro Lys Tyr Asn Thr
115 120 125

25 Phe Lys Glu Ala Leu Lys Gln Arg Asp Gly Ile Ala Val Ile Gly Ile
130 135 140

30 Phe Leu Lys Ile Gly His Glu Asn Gly Glu Phe Gln Ile Phe Leu Asp
145 150 155 160

35 Ala Leu Asp Lys Ile Lys Thr Lys Gly Lys Glu Ala Pro Phe Thr Lys
165 170 175

40 Phe Asp Pro Ser Cys Leu Phe Pro Ala Cys Arg Asp Tyr Trp Thr Tyr
180 185 190

45 Gln Gly Ser Phe Thr Thr Pro Pro Cys Glu Glu Cys Ile Val Trp Leu
195 200 205

50 Leu Leu Lys Glu Pro Met Thr Val Ser Ser Asp Gln Met Ala Lys Leu
210 215 220

55 Arg Ser Leu Leu Ser Ser Ala Glu Asn Glu Pro Pro Val Pro Leu Val
225 230 235 240

60 Ser Asn Trp Arg Pro Pro Gln Pro Ile Asn Asn Arg Val Val Arg Ala
245 250 255

65 Ser Phe Lys

<210> 26

<211> 260

<212> PRT

<213> Homo sapiens

<220>

<221> Gene

<222> (1)..(260)

<223> Carbonic anhydrase domain of human carbonic anhydrase I

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Ala Ser Pro Asp Trp Gly Tyr Asp Asp Lys Asn Gly Pro Glu Gln Trp
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Ser Lys Leu Tyr Pro Ile Ala Asn Gly Asn Asn Gln Ser Pro Val Asp
20 25 30

Ile Lys Thr Ser Glu Thr Lys His Asp Thr Ser Leu Lys Pro Ile Ser
35 40 45

Val Ser Tyr Asn Pro Ala Thr Ala Lys Glu Ile Ile Asn Val Gly His
50 55 60

Ser Phe His Val Asn Phe Glu Asp Asn Asp Asn Arg Ser Val Leu Lys
65 70 75 80

Gly Gly Pro Phe Ser Asp Ser Tyr Arg Leu Phe Gln Phe His Phe His
85 90 95

Trp Gly Ser Thr Asn Glu His Gly Ser Glu His Thr Val Asp Gly Val
100 105 110

Lys Tyr Ser Ala Glu Leu His Val Ala His Trp Asn Ser Ala Lys Tyr
115 120 125

Ser Ser Leu Ala Glu Ala Ala Ser Lys Ala Asp Gly Leu Ala Val Ile
130 135 140

Gly Val Leu Met Lys Val Gly Glu Ala Asn Pro Lys Leu Gln Lys Val
145 150 155 160

Leu Asp Ala Leu Gln Ala Ile Lys Thr Lys Gly Lys Arg Ala Pro Phe
165 170 175

Thr Asn Phe Asp Pro Ser Thr Leu Leu Pro Ser Ser Leu Asp Phe Trp
180 185 190

Thr Tyr Pro Gly Ser Leu Thr His Pro Pro Leu Tyr Glu Ser Val Thr
195 200 205

Trp Ile Ile Cys Lys Glu Ser Ile Ser Val Ser Ser Glu Gln Leu Ala
210 215 220

Gln Phe Arg Ser Leu Leu Ser Asn Val Glu Gly Asp Asn Ala Val Pro
225 230 235 240

Met Gln His Asn Asn Arg Pro Thr Gln Pro Leu Lys Gly Arg Thr Val
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Arg Ala Ser Phe
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<223> Carbonic anhydrase domain of human carbonic anhydrase VIX

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Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln Asp His
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35 40 45

10 Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp Leu Pro Ala Leu
50 55 60

15 Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu Pro Leu Asp Leu His
65 70 75 80

20 Asn Asn Gly His Thr Val Gln Leu Ser Leu Pro Ser Thr Leu Tyr Leu
85 90 95

25 Gly Gly Leu Pro Arg Lys Tyr Val Ala Ala Gln Leu His Leu His Trp
100 105 110

30 Gly Gln Lys Gly Ser Pro Gly Gly Ser Glu His Gln Ile Asn Ser Glu
115 120 125

35 Ala Thr Phe Ala Glu Leu His Ile Val His Tyr Asp Ser Asp Ser Tyr
130 135 140

40 Asp Ser Leu Ser Glu Ala Ala Glu Arg Pro Gln Gly Leu Ala Val Leu
145 150 155 160

45 Gly Ile Leu Ile Glu Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His
165 170 175

50 Ile Leu Ser His Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser
180 185 190

55 Val Pro Pro Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln
195 200 205

Tyr Phe Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser
210 215 220

Val Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
225 230 235 240

Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro Ser
245 250 255

5 Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn Gln Arg
260 265 270

10 Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr Thr Thr Gly
275 280 285

15 Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly Cys Leu Cys Leu
290 295 300

Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile Arg Lys Lys Arg Leu
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<210> 34

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<212> DNA

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22

<210> 35

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ctctgcactt cctggtaaaa ctct

24

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